and preferred embodiments should not be construed to limit the present invention to only the explicitly described embodiments. This description should be understood to support and encompass embodiments which combine two or more of the explicitly described embodiments or which combine the one or more of the explicitly described embodiments with any number of the disclosed and/or preferred elements. Furthermore, any permutations and combinations of all described elements in this application should be considered disclosed by the description of the present application unless the context indicates otherwise.

[0015] In a first aspect, the present invention relates to a method of identifying a protein kinase inhibitor for normalizing post-transcriptional regulation as precision cancer therapy comprising the following steps:

[0016] a. transfecting cancer cells or a tissue of a cancer patient with at least one expression vector comprising:

[0017] i. a promoter region comprising a non-inducible constitutively active ribosomal protein gene promoter, preferably a promoter that comprises a modified promoter of the human RPS30 gene that has the nucleic acid sequence of SEQ ID NO: 3 (RPS30M1) or SEQ ID NO:4 (RPS30M-truncated),

[0018] ii. a reporter gene; and

[0019] iii. a 3' untranslated region (3' UTR) containing an AU-rich element, wherein said reporter gene is operably linked to said promoter region and said 3' UTR.

[0020] b. providing one or more protein kinase inhibitor (s) to be tested;

[0021] c. incubating the cells or a tissue created in step a. with said one or more protein kinase inhibitor(s) to be tested;

[0022] d. determining a normalizing effect of said one or more protein kinase inhibitor(s) on post-transcriptional regulation by determining a reporter activity, wherein a reduction in reporter activity indicates that said one or more protein kinase inhibitor(s) is/are suitable for targeted cancer therapy, wherein, preferably, the reduction is a reduction by at least 15%, preferably by at least 20%, more preferably by at least 25%.

[0023] In one embodiment, the precision cancer therapy is a pan-cancer precision oncology therapy capable of treating a cancer regardless of the tissue type or subtype or molecular sub-type of the cancer including but not limited to solid tumors, hematological tumors, leukemias, lymphomas, organ-specific tumors such as breast, colon, prostate, liver, and metastatic tumors of any origin, including subtypes such as hormone positive, hormone negative, Microsatellite Instability high or low, and p53 mutant cancer.

[0024] In one embodiment, the precision cancer therapy is a universal single assay.

[0025] In one embodiment, said protein kinase inhibitor is co-administered with a chemotherapeutic agent, checkpoint inhibitor, therapeutic monoclonal antibody, interferon, cytokine inhibitor, and/or any small molecule drug, wherein, preferably, said co-administration is performed after the protein kinase inhibitor has been identified in the method of identifying according to the present invention, i.e. the co-administration is performed during the actual cancer therapy, or as part of such cancer therapy.

[0026] In one embodiment, said checkpoint inhibitor is selected from CTLA-4, PD-1, and PD-L1 targeting agents.

[0027] In one embodiment, said checkpoint inhibitor is selected from the group consisting of ipilimumab, tremelimumab, nivolumab, MK-3475, MPDL-3280A, MEDI-4736, and BMS-936559.

[0028] In one embodiment, in said precision cancer therapy, a cancer-related gene is post-transcriptionally normalized by administering said protein kinase inhibitor.

[0029] In one embodiment, in said precision cancer therapy, a gene encoding a proinflammatory cytokine is post-transcriptionally normalized by administering said protein kinase inhibitor.

[0030] In one embodiment, said administering of said protein kinase inhibitor results in the reduction of expression of a mRNA comprising an AU-rich element.

[0031] In one embodiment, said protein kinase inhibitor is selected from inhibitors of kinases of which a kinase activity is aberrant in cancer.

[0032] In one embodiment, said one or more protein kinase inhibitor(s) are any of Table 1.

[0033] In one embodiment, said more protein kinase inhibitors are a protein kinase inhibitor library.

[0034] In one embodiment, said reporter activity is detected by measuring a mRNA level, and/or the expression level of the reporter gene, and/or the activity of the reporter, wherein the expression of said reporter gene is independent of transcriptional induction.

[0035] In this aspect, said protein kinase inhibitor, said cancer, said cancer cells, and said patient are as defined below.

[0036] In a further aspect, the present invention relates to a method of treatment of cancer in a patient, wherein said cancer is characterized by one of the following:

[0037] underexpression of TTP and overexpression of HuR,

[0038] underexpression of TTP and overexpression of PLK-1,

[0039] overexpression of HuR and overexpression of PLK-1,

[0040] underexpression of TTP and overexpression of HuR and overexpression of PLK-1,

[0041] in cancer cells compared to expression in non-cancerous cells;

said method comprising administering an effective dose of a protein kinase inhibitor to a patient in need thereof having said cancer, wherein said protein kinase inhibitor is a B-Raf kinase inhibitor, VEGFR2 inhibitor, or polo-like kinase inhibitor, preferably a polo-like kinase 1 inhibitor.

[0042] In one embodiment, said method comprises the steps of:

[0043] a. Receiving a sample of a tumor (tumor sample), and optionally a control sample, from the patient,

[0044] b. Determining the level of expression of TTP, and/or HuR, and/or PLK-1 in said tumor sample, and optionally in said control sample,

[0045] c. Administering a therapeutically effective amount of said protein kinase inhibitor, preferably of said polo-like kinase inhibitor (PLK), more preferably a PLK-1 inhibitor to the patient, if there is a reduced expression of TTP and/or increased expression of HuR, and/or increased expression of PLK-1 in the tumor sample as compared to a control sample, which is optionally the control sample of said patient, as determined in step b).